

SEQUENCE LISTING

<110> University of Utah

<120> HEPARIN BINDING PROTEINS: SENSORS FOR
HEPARIN DETECTION

<130> 21101.0041P1

<140> Unassigned

<141> 2004-08-12

<150> 60/494,495

<151> 2003-08-12

<160> 67

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<221> VARIANT

<222> 1,9

<223> Xaa can be Arg or Lys

<221> VARIANT

<222> 2-8

<223> Xaa = basic residues

<400> 1

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 2

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 2

cgggatccgg tgctagccgt gactcctatg cacagctcct tgg

43

<210> 3

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 3
ggagcggtcg acacggatgc ccagagctt atctaattc 39

<210> 4
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 4
gatccggctcg agaggaaat ggttctggaa gtggttcagg ttcgggttagc ggatctggtt 60
caggaagtgg tt 72

<210> 5
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 5
ctagaaccac ttccctgaacc agatccgcta cccgaacctg aaccacttcc agaaccactt 60
ccctcgagac cg 72

<210> 6
<211> 62
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 6
Arg Asp Ser Tyr Ala Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys
1 5 10 15
Ile Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser
20 25 30
Glu Val Ser Lys Leu Arg Ser Gln Leu Val Lys Arg Lys Gln Asn Glu
35 40 45
Leu Arg Leu Gln Gly Glu Leu Asp Lys Ala Leu Gly Ile Arg
50 55 60

<210> 7
<211> 794
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 7

Met Ser Phe Pro Lys Ala Pro Leu Lys Arg Phe Asn Asp Pro Ser Gly
 1 5 10 15
 Cys Ala Pro Ser Pro Gly Ala Tyr Asp Val Lys Thr Ser Glu Ala Thr
 20 25 30
 Lys Gly Pro Val Ser Phe Gln Lys Ser Gln Arg Phe Lys Asn Gln Arg
 35 40 45
 Glu Ser Gln Gln Asn Leu Ser Ile Asp Lys Asp Thr Thr Leu Leu Ala
 50 55 60
 Ser Ala Lys Lys Ala Lys Lys Ser Val Ser Lys Lys Asp Ser Gln Lys
 65 70 75 80
 Asn Asp Lys Asp Val Lys Arg Leu Glu Lys Glu Ile Arg Ala Leu Leu
 85 90 95
 Gln Glu Arg Gly Thr Gln Asp Lys Arg Ile Gln Asp Met Glu Ser Glu
 100 105 110
 Leu Glu Lys Thr Glu Ala Lys Leu Asn Ala Ala Val Arg Glu Lys Thr
 115 120 125
 Ser Leu Ser Ala Ser Asn Ala Ser Leu Glu Lys Arg Leu Thr Glu Leu
 130 135 140
 Thr Arg Ala Asn Glu Leu Leu Lys Ala Lys Phe Ser Glu Asp Gly His
 145 150 155 160
 Gln Lys Asn Met Arg Ala Leu Ser Leu Glu Leu Met Lys Leu Arg Asn
 165 170 175
 Lys Arg Glu Thr Lys Met Arg Ser Met Met Val Lys Gln Glu Gly Met
 180 185 190
 Glu Leu Lys Leu Gln Ala Thr Gln Lys Asp Leu Thr Glu Ser Lys Gly
 195 200 205
 Lys Ile Val Gln Leu Glu Gly Lys Leu Val Ser Ile Glu Lys Glu Lys
 210 215 220
 Ile Asp Glu Lys Cys Glu Thr Glu Lys Leu Leu Glu Tyr Ile Gln Glu
 225 230 235 240
 Ile Ser Cys Ala Ser Asp Gln Val Glu Lys Cys Lys Val Asp Ile Ala
 245 250 255
 Gln Leu Glu Glu Asp Leu Lys Glu Lys Asp Arg Glu Ile Leu Ser Leu
 260 265 270
 Lys Gln Ser Leu Glu Glu Asn Ile Thr Phe Ser Lys Gln Ile Glu Asp
 275 280 285
 Leu Thr Val Lys Cys Gln Leu Leu Glu Thr Glu Arg Asp Asn Leu Val
 290 295 300
 Ser Lys Asp Arg Glu Arg Ala Glu Thr Leu Ser Ala Glu Met Gln Ile
 305 310 315 320
 Leu Thr Glu Arg Leu Ala Leu Glu Arg Gln Glu Tyr Glu Lys Leu Gln
 325 330 335
 Gln Lys Glu Leu Gln Ser Gln Ser Leu Leu Gln Gln Glu Lys Glu Leu
 340 345 350
 Ser Ala Arg Leu Gln Gln Leu Cys Ser Phe Gln Glu Glu Met Thr
 355 360 365
 Ser Glu Lys Asn Val Phe Lys Glu Glu Leu Lys Leu Ala Leu Ala Glu
 370 375 380
 Leu Asp Ala Val Gln Gln Lys Glu Glu Gln Ser Glu Arg Leu Val Lys
 385 390 395 400
 Gln Leu Glu Glu Glu Arg Lys Ser Thr Ala Glu Gln Leu Thr Arg Leu
 405 410 415
 Asp Asn Leu Leu Arg Glu Lys Glu Val Glu Leu Glu Lys His Ile Ala
 420 425 430
 Ala His Ala Gln Ala Ile Leu Ile Ala Gln Glu Lys Tyr Asn Asp Thr
 435 440 445
 Ala Gln Ser Leu Arg Asp Val Thr Ala Gln Leu Glu Ser Val Gln Glu
 450 455 460
 Lys Tyr Asn Asp Thr Ala Gln Ser Leu Arg Asp Val Thr Ala Gln Leu
 465 470 475 480

Glu Ser Glu Gln Glu Lys Tyr Asn Asp Thr Ala Gln Ser Leu Arg Asp
 485 490 495
 Val Thr Ala Gln Leu Glu Ser Glu Gln Glu Lys Tyr Asn Asp Thr Ala
 500 505 510
 Gln Ser Leu Arg Asp Val Thr Ala Gln Leu Glu Ser Val Gln Glu Lys
 515 520 525
 Tyr Asn Asp Thr Ala Gln Ser Leu Arg Asp Val Ser Ala Gln Leu Glu
 530 535 540
 Ser Tyr Lys Ser Ser Thr Leu Lys Glu Ile Glu Asp Leu Lys Leu Glu
 545 550 555 560
 Asn Leu Thr Leu Gln Glu Lys Val Ala Met Ala Glu Lys Ser Val Glu
 565 570 575
 Asp Val Gln Gln Gln Ile Leu Thr Ala Glu Ser Thr Asn Gln Glu Tyr
 580 585 590
 Ala Arg Met Val Gln Asp Leu Gln Asn Arg Ser Thr Leu Lys Glu Glu
 595 600 605
 Glu Ile Lys Glu Ile Thr Ser Ser Phe Leu Glu Lys Ile Thr Asp Leu
 610 615 620
 Lys Asn Gln Leu Arg Gln Gln Asp Glu Asp Phe Arg Lys Gln Leu Glu
 625 630 635 640
 Glu Lys Gly Lys Arg Thr Ala Glu Lys Glu Asn Val Met Thr Glu Leu
 645 650 655
 Thr Met Glu Ile Asn Lys Trp Arg Leu Leu Tyr Glu Glu Leu Tyr Glu
 660 665 670
 Lys Thr Lys Pro Phe Gln Gln Leu Asp Ala Phe Glu Ala Glu Lys
 675 680 685
 Gln Ala Leu Leu Asn Glu His Gly Ala Thr Gln Glu Gln Leu Asn Lys
 690 695 700
 Ile Arg Asp Ser Tyr Ala Gln Leu Leu Gly His Gln Asn Leu Lys Gln
 705 710 715 720
 Lys Ile Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys
 725 730 735
 Ser Glu Val Ser Lys Leu Arg Ser Gln Leu Val Lys Arg Lys Gln Asn
 740 745 750
 Glu Leu Arg Leu Gln Gly Glu Leu Asp Lys Ala Leu Gly Ile Arg His
 755 760 765
 Phe Asp Pro Ser Lys Ala Phe Cys His Ala Ser Lys Glu Asn Phe Thr
 770 775 780
 Pro Leu Lys Glu Gly Asn Pro Asn Cys Cys
 785 790

<210> 8

<211> 3539

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 8

tcaggcgagc	tgacagtttgc	ctggggcggtt	tgattgctgt	ctcatctggaa	cccaggcgtc	60
agaatgtcct	ttccttaaggc	gcccctgaag	agattcaatg	acccttcggg	ttgtgctcca	120
tctccgggttgc	cttatgtatgt	taaaaacttca	gaagcaacta	aaggaccagt	gtcttttcag	180
aaatcacaaa	gattttaaaaaa	ccaaaagagag	tctcaacaaa	atcttagcat	tgacaaaagat	240
acaacaccttgc	ttgcttcggc	taaaaaagca	aagaagtctg	tgtcaaagaa	ggactctcag	300
aagaatgata	aagatgtgaa	gagattagaa	aaagagattc	gcgcttttt	gcaagagcga	360
gggacttcagg	acaaaacggat	ccaggacatg	gaatctgaat	tggagaagac	agaagcaaag	420
ctcaatgcag	cagtcagaga	gaaaacatct	ctctctgcga	gtaatgcttc	actggaaaaaa	480
cggcttactg	aattaaccag	agccaaacgag	ctactaaagg	ctaagtttc	tgaagatgg	540
caccaaaaga	atataaccggc	tctaaaggctg	gaattgtatga	aactcagaaa	taagagagag	600

acaaggatga	ggagttatgtat	ggtcaaacag	gaaggcatgg	agctgaagct	gcaggccact	660
cagaaggacc	tcaacggagtc	taaggaaaa	atagtccagc	tggagggaaa	gcttgttca	720
atagagaaaag	aaaagatcga	tgaaaaatgt	gaaacagaaa	aactctttaga	atacatccaa	780
gaaatttagct	gtgcatctga	tcaagtggaa	aatgc当地	tagatattgc	ccagttagaa	840
gaagatttga	aagagaagga	tcgtgagatt	ttaagtctt	agcagtctct	tgagggaaaac	900
attacatttt	ctaagcaa	agaagacctg	actgttaaaat	gccagctact	tgaaacagaa	960
agagacaacc	ttgtcagcaa	ggatagagaa	agggctgaaa	ctctcagtg	tgagatgcag	1020
atcctgacag	agaggctggc	tctggaaaagg	caagaatatg	aaaagctgca	acaaaaagaa	1080
ttgcaaagcc	agtca	gcagcaagag	aaggaactgt	ctgctcgtct	gcagcagcag	1140
ctctgctt	tccaagagga	aatgacttct	gagaagaaacg	tctttaaga	agagctaaag	1200
ctcgccctgg	ctgagttgga	tgcggtccag	cagaaggagg	agcagagtga	aaggctgg	1260
aaacagctgg	aagaggaaaag	gaagtcact	gcagaacaac	tgacgcggct	ggacaacctg	1320
ctgagagaga	aagaagtgt	actggagaaa	catattgt	ctcacgccc	agccatctt	1380
attgcacaag	agaagtataa	tgacacagca	cagagtctga	gggacgtcac	tgctcagtt	1440
gaaagtgtgc	aagagaagta	taatgacaca	gcacagagtc	tgagggacgt	cactgctcag	1500
ttggaaaagt	agcaagagaa	gtacaatgac	acagcacaga	gtctgaggga	cgtcactgct	1560
cagttggaaa	gtgagcaaga	gaagtacaat	gacacagcac	agagtcttag	ggacgtcact	1620
gctcagt	aaagtgtgc	agagaagtac	aatgacacag	cacagagtct	gagggacgtc	1680
agtgc	tggaaagct	taagtcatca	acacttaaaag	aaatagaaga	tcttaactg	1740
gagaatttga	ctctacaaga	aaaagtagct	atggctgaaa	aaagtgtaga	agatgtcaa	1800
cagcagat	tgacagctga	gagcacaat	caagaatatg	caaggatgt	tcaagattt	1860
cagaacagat	caaccttaaa	agaagaagaa	attaaagaaa	tcacatctt	atttcttgag	1920
aaaataactg	atttggaaa	tcaactcaga	caacaagatg	aagactttag	gaagcagctg	1980
gaagagaaaag	gaaaaagaac	agcagagaaa	gaaaatgtaa	tgacagaatt	aaccatggaa	2040
attaataat	ggcgtctcct	atatgaa	ctatataaaa	aaactaaacc	ttttcagcaa	2100
caactggat	cctttaagc	cgagaaacag	gcattgttga	atgaacatgg	tgcaactcag	2160
gagcagctaa	ataaaaatcag	agactcctat	gcacagctac	ttggtcacca	gaacctaaag	2220
caaaaaatca	aacatgtt	gaaatgaaa	gatgaaaata	gccaaactca	atcgagggt	2280
tcaaaactcc	gatctcagct	tgtaaaagg	aaacaaaatg	agctcagact	tcagggagaa	2340
tttagataaag	ctctggcat	cagacactt	gacccttcca	aggctttt	tcatgcac	2400
aaggagaatt	ttactccatt	aaaagaaggc	aacccaaact	gctgctgagt	tcagatcaa	2460
cttcaagaat	catggaa	tacgtctgaa	atacttgtt	aagattattt	tcttcattgt	2520
tcttgcatt	atgtttatag	tatataattat	ataatgtatt	taatttctac	tgccctagtt	2580
taggtat	aaacggtaat	tcagcattt	ttctctgtt	tagtcagggt	ttctgttct	2640
gcataaaat	cagaccaaga	aacaagctgg	ggaggaaaagg	gttattcag	cttacactt	2700
catactgct	ttcatcacca	aaggaagtca	ggactggaa	tcaagcaggt	caggaagttag	2760
gagctgat	agaggccat	gagggacatt	ccttactggc	ttgcttcccc	tggcttgc	2820
agcttgc	cttacagaac	ccaagtctac	cagcctagag	acagcacaa	ccacaagggg	2880
ccctccacc	cttgatcaat	aattgagaaa	aatgccttac	agttggatct	catgaaggca	2940
ttttctcacc	tgaagctcct	tctctgtat	aactccaggt	ggtgtcaagt	tgacacacaa	3000
acacattact	attaagcctc	aacccttact	ttcttattaa	tcccatgtat	aaaataact	3060
ttaaaaagtcc	cacagtctt	gaaaattctt	aaatcttca	tccctttaaa	atatccaaatc	3120
tcttttaaaa	ttcaaaagtct	tttacaatt	aaaagtctc	ttaactgtgg	tctccactaa	3180
aatactttct	tccttcaaga	ggggaaaata	tcagggcaca	gtcacaacaa	attaaaagca	3240
aaatcaaact	acaacctca	acgtctggg	ccctccaagg	gcttgggtca	ttctcttagc	3300
tctgcctt	gtagcacaca	agttgtctc	taggtccag	atgcctgtac	tccactgctg	3360
ctgcttct	tggta	ttatgtact	gcatctcca	aaacactgtt	gtctttgctg	3420
taacttaggct	tcaccaatag	cctctcatag	gctcttttca	tggtgccaag	cctcaaatcc	3480
tttgaatgac	cccttca	ttggccatc	aactgctact	gaggctgcac	ttggaaattc	3539

<210> 9
<211> 631
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 9

Met Arg Ala Leu Ser Leu Glu Leu Met Lys Leu Arg Asn Lys Arg Glu
 1 5 10 15
 Thr Lys Met Arg Ser Met Met Val Lys Gln Glu Gly Met Glu Leu Lys
 20 25 30
 Leu Gln Ala Thr Gln Lys Asp Leu Thr Glu Ser Lys Gly Lys Ile Val
 35 40 45
 Gln Leu Glu Gly Lys Leu Val Ser Ile Glu Lys Glu Lys Ile Asp Glu
 50 55 60
 Lys Cys Glu Thr Glu Lys Leu Leu Glu Tyr Ile Gln Glu Ile Ser Cys
 65 70 75 80
 Ala Ser Asp Gln Val Glu Lys Cys Lys Val Asp Ile Ala Gln Leu Glu
 85 90 95
 Glu Asp Leu Lys Glu Lys Asp Arg Glu Ile Leu Ser Leu Lys Gln Ser
 100 105 110
 Leu Glu Glu Asn Ile Thr Phe Ser Lys Gln Ile Glu Asp Leu Thr Val
 115 120 125
 Lys Cys Gln Leu Leu Glu Thr Glu Arg Asp Asn Leu Val Ser Lys Asp
 130 135 140
 Arg Glu Arg Ala Glu Thr Leu Ser Ala Glu Met Gln Ile Leu Thr Glu
 145 150 155 160
 Arg Leu Ala Leu Glu Arg Gln Glu Tyr Glu Lys Leu Gln Gln Lys Glu
 165 170 175
 Leu Gln Ser Gln Ser Leu Leu Gln Glu Lys Glu Leu Ser Ala Arg
 180 185 190
 Leu Gln Gln Gln Leu Cys Ser Phe Gln Glu Glu Met Thr Ser Glu Lys
 195 200 205
 Asn Val Phe Lys Glu Glu Leu Lys Leu Ala Leu Ala Glu Leu Asp Ala
 210 215 220
 Val Gln Gln Lys Glu Glu Gln Ser Glu Arg Leu Val Lys Gln Leu Glu
 225 230 235 240
 Glu Glu Arg Lys Ser Thr Ala Glu Gln Leu Thr Arg Leu Asp Asn Leu
 245 250 255
 Leu Arg Glu Lys Glu Val Glu Leu Glu Lys His Ile Ala Ala His Ala
 260 265 270
 Gln Ala Ile Leu Ile Ala Gln Glu Lys Tyr Asn Asp Thr Ala Gln Ser
 275 280 285
 Leu Arg Asp Val Thr Ala Gln Leu Glu Ser Val Gln Glu Lys Tyr Asn
 290 295 300
 Asp Thr Ala Gln Ser Leu Arg Asp Val Thr Ala Gln Leu Glu Ser Glu
 305 310 315 320
 Gln Glu Lys Tyr Asn Asp Thr Ala Gln Ser Leu Arg Asp Val Thr Ala
 325 330 335
 Gln Leu Glu Ser Glu Gln Glu Lys Tyr Asn Asp Thr Ala Gln Ser Leu
 340 345 350
 Arg Asp Val Thr Ala Gln Leu Glu Ser Val Gln Glu Lys Tyr Asn Asp
 355 360 365
 Thr Ala Gln Ser Leu Arg Asp Val Ser Ala Gln Leu Glu Ser Tyr Lys
 370 375 380
 Ser Ser Thr Leu Lys Glu Ile Glu Asp Leu Lys Leu Glu Asn Leu Thr
 385 390 395 400
 Leu Gln Glu Lys Val Ala Met Ala Glu Lys Ser Val Glu Asp Val Gln
 405 410 415
 Gln Gln Ile Leu Thr Ala Glu Ser Thr Asn Gln Glu Tyr Ala Arg Met
 420 425 430
 Val Gln Asp Leu Gln Asn Arg Ser Thr Leu Lys Glu Glu Ile Lys
 435 440 445
 Glu Ile Thr Ser Ser Phe Leu Glu Lys Ile Thr Asp Leu Lys Asn Gln
 450 455 460

Leu Arg Gln Gln Asp Glu Asp Phe Arg Lys Gln Leu Glu Glu Lys Gly
 465 470 475 480
 Lys Arg Thr Ala Glu Lys Glu Asn Val Met Thr Glu Leu Thr Met Glu
 485 490 495
 Ile Asn Lys Trp Arg Leu Leu Tyr Glu Glu Leu Tyr Glu Lys Thr Lys
 500 505 510
 Pro Phe Gln Gln Gln Leu Asp Ala Phe Glu Ala Glu Lys Gln Ala Leu
 515 520 525
 Leu Asn Glu His Gly Ala Thr Gln Glu Gln Leu Asn Lys Ile Arg Asp
 530 535 540
 Ser Tyr Ala Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys Ile Lys
 545 550 555 560
 His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser Glu Val
 565 570 575
 Ser Lys Leu Arg Ser Gln Leu Val Lys Arg Lys Gln Asn Glu Leu Arg
 580 585 590
 Leu Gln Gly Glu Leu Asp Lys Ala Leu Gly Ile Arg His Phe Asp Pro
 595 600 605
 Ser Lys Ala Phe Cys His Ala Ser Lys Glu Asn Phe Thr Pro Leu Lys
 610 615 620
 Glu Gly Asn Pro Asn Cys Cys
 625 630

<210> 10

<211> 3167

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 10

aggccttagg	tccaggaagg	aggaaaaacc	atcttcttct	ctgcgagtaa	tgcttcactg	60
gtaaaaacgg	cttactgaat	taaccagagc	caacgagcta	ctaaaaggct	aaaggaggca	120
gaatagat	ctgagttctt	atgtttattg	tagtttctg	aagatggtca	ccaaaagaat	180
atgagagctc	taagcctgga	attgatgaaa	ctcagaaata	agagagagac	aaagatgagg	240
agtatgatgg	tcaaacagga	aggcatggag	ctgaagctgc	aggccactca	gaaggacctc	300
acggagtcta	agggaaaaat	agtccagctg	gagggaaagc	ttgtttcaat	agagaaagaa	360
aagatcgatg	aaaaatgtga	aacagaaaaa	ctcttagaat	acatccaaga	aattagctgt	420
gcatctgatc	aagtggaaaa	atgcaaagta	gatattgcc	agttagaaga	agatttggaaa	480
gagaaggatc	gtgagattt	aagtcttaag	cagtctcttg	äggaääacat	tacatttct	540
aagcaaata	agacccgtac	tgttaaatgc	cagctacttg	aaacagaaaag	agacaacctt	600
gtcagcaagg	atagagaaag	ggctgaaact	ctcagtgctg	agatgcagat	cctgacagag	660
aggctggctc	tggaaaggca	agaatatgaa	aagctgcaac	aaaaagaatt	gcaaagccag	720
tcacttctgc	agcaagagaa	ggaactgtct	gctcgctgc	agçagcagct	ctgctcttgc	780
caagaggaaa	tgacttctga	gaagaacgtc	tttaaagaag	agctaaagct	cgcctggct	840
gagttggatg	cggtccagca	gaaggaggag	cagagtggaa	ggctggtaa	acagctggaa	900
gaggaaagga	agtcaactgc	agaacaactg	acgcggctgg	acaacctgct	gagagagaaa	960
gaagttgaac	tggagaaaca	tattgtctgt	cacccccaa	ccatcttgat	tgccacaagag	1020
aagtataatg	acacagcaca	gagtctgagg	gacgtcaactg	ctcagttgga	aagtgtgcaa	1080
gagaagtata	atgacacacgc	acagagtctg	agggacgtca	ctgctcagtt	ggaaaagttag	1140
caagagaagt	acaatgacac	agcacagagt	ctgagggacg	tcactgtc	gttggaaaagt	1200
gagcaagaga	agtacaatga	cacagcacag	agtctgaggg	acgtcactgc	tcagttggaa	1260
agtgtgcaag	agaagtacaa	tgacacacga	cagagtctga	gggacgtcag	tgctcagtt	1320
gaaagctata	agtcatcaac	acttaaagaa	atagaagatc	ttaaactgg	gaatttgact	1380
ctacaagaaa	aagttagctat	ggctgaaaaa	agttagaaag	atgttcaaca	gcagatattg	1440
acagctgaga	gcacaaatca	agaatatgca	aggatggtc	aagatttgca	gaacagatca	1500
accttaaaag	aagaagaaat	taaagaaatc	acatcttcat	ttcttgagaa	aataactgat	1560
ttgaaaaato	aactcagaca	acaagatgaa	gactttagga	agcagctgga	agagaaagga	1620
aaaagaacag	cagagaaaaga	aaatgtaatg	acagaattaa	ccatggaaat	taataaatgg	1680

cgtctcctat atgaagaact atatgaaaaa actaaacctt ttcagcaaca actggatgcc	1740
tttgaagccg agaaacaggc attgttgaat gaacatggtg caactcagga gcagctaaat	1800
aaaatcagag actcctatgc acagctactt ggtcaccaga acctaaagca aaaaatcaaa	1860
catgttgtga aattgaaaga tgaaaatagc caactcaa at cggaggtgtc aaaactccga	1920
tctcagctt taaaaggaa acaaaatgag ctcagactt c agggagaatt agataaagct	1980
ctggcatca gacacttga cccttccaag gcttttgc atgcataa ggagaatttt	2040
actccattaa aagaaggcaa cccaaactgc tgctgagttc agatgcaact tcaagaatca	2100
tggaagtata cgtctgaaat acttgttga gattatttc ttcatgttc ttgatattat	2160
gtttatagta tatattat aatgtattt atttctactg cctagtctt ggtatatgaa	2220
acgtaattc agcattgtt ctctgtctt gtcagggtt ctgttctgc ataaacatca	2280
gaccaagaaa caagctggg aggaaagggt ttattcagct tacacttcca tactgctgtt	2340
catcaccaaa ggaagtcaagg actggaactc aagcaggtca ggaagttagga gctgatgcag	2400
aggccatggg gggacattcc ttactggtt gcttcccctg gcttgctcag ctgctttct	2460
tacagaaccc aagtctacca gcctagagac agcaccaacc acaaggggcc ctcccacccct	2520
tgatcaataa ttgagaaaaa tgccttacag ttggatctca tgaaggcatt ttctcacctg	2580
aagctccttc tctgtgataa ctccaggtgg tgtcaagttg acacacaaaac acattactat	2640
taagcctcaa cccttacttt cttattaatc cccatgatca aaataacttt aaaagtccca	2700
cagtcttga aaattcttaa aatttcaatc cctttaaat atccaatctc tttaaaatt	2760
caaagtcttt ttacaattaa aaagtcttt aactgtggtc tccactaaaa tactttcttc	2820
cttcaagagg gaaaaatatc agggcacagt cacaaacaat taaaagcaaa atcaaactac	2880
aacctcaaacc gtctgggacc ctccaaggc ttgggtcact tctctagctc tgccctttgt	2940
agcacacaaag ttgtcttcta ggctccagat gcctgtactc cactgctgct gctgttcttg	3000
gtactcattt atggtaactgg catctccaaa acactgttgc ttgtctgta actaggcttc	3060
accaatagcc tctcatagcc tctcttcatg gtgccaagcc tcaaattctt tgaatgaccc	3120
cttcagtctt gggccatcaa ctgtactga ggctgcactt ggaattc	3167

<210> 11

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 11

Met Gly Gly Gly Val Ser Tyr Val Gly Trp Leu Glu Lys Ser Glu Thr
1 5 10 15Glu Lys Leu Leu Glu Tyr Ile Glu Glu Ile Ser Cys Ala Ser Asp Gln
20 25 30Val Glu Lys Tyr Lys Leu Asp Ile Ala Gln Leu Glu Glu Asp Leu Lys
35 40 45Glu Lys Asp Arg Glu Ile Leu Cys Leu Lys Gln Ser Leu Glu Glu Lys
50 55 60Val Ser Phe Ser Lys Gln Ile Glu Asp Leu Thr Val Lys Cys Gln Leu
65 70 75 80Leu Glu Ala Glu Arg Asp Asp Leu Val Ser Lys Asp Arg Glu Arg Ala
85 90 95Glu Ser Leu Ser Ala Glu Met Gln Val Leu Thr Glu Lys Leu Leu Leu
100 105 110Glu Arg Gln Glu Tyr Glu Lys Leu Gln Gln Asn Glu Leu Gln Ser Gln
115 120 125Ser Leu Leu Gln Gln Glu Lys Glu Leu Ser Ala His Leu Gln Gln Gln
130 135 140

Leu Cys Ser Phe Gln Glu Met Thr Ser Glu Arg Asn Val Phe Lys

145 150 155 160

Glu Gln Leu Lys Leu Ala Leu Asp Glu Leu Asp Ala Val Gln Gln Lys
165 170 175

Glu Glu Gln Ser Glu Lys Leu Val Lys Gln Leu Glu Glu Glu Thr Lys
 180 185 190
 Ser Thr Ala Glu Gln Leu Arg Arg Leu Asp Asp Leu Leu Arg Glu Lys
 195 200 205
 Glu Ile Glu Leu Glu Lys Arg Thr Ala Ala His Ala Gln Ala Thr Val
 210 215 220
 Ile Ala Gln Glu Lys Tyr Ser Asp Thr Ala Gln Thr Leu Arg Asp Val
 225 230 235 240
 Thr Ala Gln Leu Glu Ser Tyr Lys Ser Ser Thr Leu Lys Glu Ile Glu
 245 250 255
 Asp Leu Lys Leu Glu Asn Leu Thr Leu Gln Glu Lys Val Ala Met Ala
 260 265 270
 Glu Lys Arg Val Glu Asp Val Gln Gln Gln Ile Leu Thr Ala Glu Ser
 275 280 285
 Thr Asn Gln Glu Tyr Ala Lys Val Val Gln Asp Leu Gln Asn Ser Ser
 290 295 300
 Thr Leu Lys Glu Ala Glu Ile Lys Glu Ile Thr Ser Ser Tyr Leu Glu
 305 310 315 320
 Lys Ile Thr Asp Leu Gln Asn Gln Leu Arg Gln Gln Asn Glu Asp Phe
 325 330 335
 Arg Lys Gln Leu Glu Glu Glu Gly Ala Lys Met Thr Glu Lys Glu Thr
 340 345 350
 Ala Val Thr Glu Leu Thr Met Glu Ile Asn Lys Trp Arg Leu Leu Tyr
 355 360 365
 Glu Glu Leu Tyr Asp Lys Thr Lys Pro Phe Gln Gln Gln Leu Asp Ala
 370 375 380
 Phe Glu Ala Glu Lys Gln Ala Leu Leu Asn Glu His Gly Ala Thr Gln
 385 390 395 400
 Glu Gln Leu Ser Lys Ile Arg Asp Ser Tyr Ala Gln Leu Leu Gly His
 405 410 415
 Gln Asn Leu Lys Gln Lys Ile Lys His Val Val Lys Leu Lys Asp Glu
 420 425 430
 Asn Ser Gln Leu Lys Ser Glu Val Ser Lys Leu Arg Ser Gln Leu Ala
 435 440 445
 Lys Arg Lys Gln Asn Glu Leu Arg Leu Gln Gly Glu Leu Asp Lys Ala
 450 455 460
 Leu Gly Ile Arg His Phe Asp Pro Pro Lys Ala Phe Cys His Glu Ser
 465 470 475 480
 Lys Glu Asn Val Thr Leu Lys Thr Pro Leu Lys Glu Gly Asn Pro Asn
 485 490 495
 Cys Cys

<210> 12
 <211> 2049
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 12
 aaccagctat caccaagctc gataggctt tcacacctac ctaaaaatct tcccaactatt 60
 ttgctacata gacgggttga ttcataat tgggttttagg tagctcggtt gggttcgggg 120
 ttcttagctt aaattctttt tgctaaggat ttcttagtta attcattatg caaaaggat 180
 aagggttaat ctttgcttat tttaacttta aattagtctt tcaccattcc cttgcggtag 240
 ttctctata gctcctggta agtaaatcc ttctccaat acttttgag ttaaatgttt 300
 tagtttatgg gggggggggt tagttatgtt ggttggttgg aaaaatctga aacagaaaaaa 360

ctcttagaat acatagaaga aattagctgt gcacatctgatc aagtggaaaa atacaaacta	420
gatattgcc agttagaaga agatttggaaa gagaaggatc gtgagatTTT atgccttaag	480
caatcttgc aggaaaaggt ttcctttct aagcaaatacg aagacctgac tggtaaatgt	540
cagctgcttgc aagcagaaag agatgatctc gtcagcaagg acagagaaag ggctgaaagc	600
ctcagtgcgt agatgcagg tctaaccagg aagctgcTTT tagaaaggca agaataatgaa	660
aagctgcaac aaaatgaatt gcaaaggccag tcacttctgc agcaagaaaa ggaactgtct	720
gctcatcttc agcagcagct ctgctcattt caagaggaaa tgacctccga gaggaatgtc	780
ttttaagaac agttgaagct tgccctggat gagctggatg ccgtccagca gaaggaggag	840
cagagtggaaa agctggatTTT acagctagaag gaggaaacgaa agtcaactgc ggaacagctg	900
aggccgctgg atgatctgcg gagagagaaa gaaattgaac tggagaaaaag aaccgctgca	960
catgcccagg ccactgtgt tgcgcaagag aagtacagtgc acacagcgca gactctgaga	1020
gatgttactg ctcagttaga aagctataag tcaccaacac taaaagaaaaat agaagatctt	1080
aaactggaga atttgactct acaagaaaaa gtagccatgg ctgagaaaaag ggtagaagat	1140
gttcaacaac aaatattaac agctgagagc acaaatacg aatatgcaaa ggtggttcaa	1200
gatttgcaga acagctcaac attgaaaagaa gcagaaatta aagaaatcac atcttcataat	1260
cttggaaaaa taactgatTTT gcaaaaatcaa ctccgacaac aaaatgaaga cttaggaag	1320
cagctggaaag aggaaggggc aaaatgaca gagaagaaaa ctgcagtgc agaattaacc	1380
atggaaatta ataaatggcg ttccttatTTT gaagaactgt atgacaaaac taaacctttt	1440
cagcaacaac tggatgcTTT cgaaggcagag aagcaggcac ttttgaatga acatggtgca	1500
actcaggagc agctaagtaa aatcagagac tcctacgcac agctgcttgg ccaccagaat	1560
ctgaagcaaa aatcaaaca tgcgtgaaa ttgaaaagatg aaaatagcca actcaaatacg	1620
gaggtgtcaa aactccgatc tcaagttgtc aaaaggaaac aaaatgagct cagacttcag	1680
ggagaattag ataaagctct gggcatcagg cactttgacc ctccctaaaggc tttttgccat	1740
gaatctaagg agaatgtgc cctcaagact ccattgaaaag aaggcaaccc gaactgctgc	1800
ttagtcagac tgcagggacc gtggaaagtgg acgtccaaga tacttgcgtga agattgttct	1860
cttcattatt cttgatattt tgttataagt atatattata taatgtatTTT aatttctact	1920
gcctattctt aggtatatga aacggtaatt caacatttgc tatcaaatacg tttttgaca	1980
ttttatTTT tattatgtgt ctcccttaatc atcacctggatc tccctcattt ctgaaccatt	2040
gcttggctt	2049

<210> 13

<211> 709

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 13

Met	Ser	Phe	Pro	Lys	Ala	Pro	Leu	Lys	Arg	Phe	Asn	Asp	Pro	Ser	Gly
1		5				10			15						
Cys	Ala	Pro	Ser	Pro	Gly	Ala	Tyr	Asp	Val	Lys	Thr	Leu	Glu	Val	Leu
	20					25				30					
Lys	Gly	Pro	Val	Ser	Phe	Gln	Lys	Ser	Gln	Arg	Phe	Lys	Gln	Gln	Lys
	35				40				45						
Glu	Ser	Lys	Gln	Asn	Leu	Asn	Val	Asp	Lys	Asp	Thr	Thr	Leu	Pro	Ala
	50				55				60						
Ser	Ala	Arg	Lys	Val	Lys	Ser	Ser	Glu	Ser	Lys	Ile	Arg	Val	Leu	Leu
	65			70			75			80					
Gln	Glu	Arg	Gly	Ala	Gln	Asp	Ser	Arg	Ile	Gln	Asp	Leu	Glu	Thr	Glu
	85				90				95						
Leu	Glu	Lys	Met	Glu	Ala	Arg	Leu	Asn	Ala	Ala	Leu	Arg	Glu	Lys	Thr
	100			105			110								
Ser	Leu	Ser	Ala	Asn	Asn	Ala	Thr	Leu	Glu	Lys	Gln	Leu	Ile	Glu	Leu
	115				120				125						
Thr	Arg	Thr	Asn	Glu	Leu	Leu	Lys	Ser	Lys	Phe	Ser	Glu	Asn	Gly	Asn
	130			135			140								
Gln	Lys	Asn	Leu	Arg	Ile	Leu	Ser	Leu	Glu	Leu	Met	Lys	Leu	Arg	Asn
	145				150			155			160				

Lys Arg Glu Thr Lys Met Arg Gly Met Met Ala Lys Gln Glu Gly Met
 165 170 175
 Glu Met Lys Leu Gln Val Thr Gln Arg Ser Leu Glu Glu Ser Gln Gly
 180 185 190
 Lys Ile Ala Gln Leu Glu Gly Lys Leu Val Ser Ile Glu Lys Glu Lys
 195 200 205

Ile Asp Glu Lys Ser Glu Thr Glu Lys Leu Leu Glu Tyr Ile Glu Glu
 210 215 220
 Ile Ser Cys Ala Ser Asp Gln Val Glu Lys Tyr Lys Leu Asp Ile Ala
 225 230 235 240
 Gln Leu Glu Glu Asn Leu Lys Glu Lys Asn Asp Glu Ile Leu Ser Leu
 245 250 255
 Lys Gln Ser Leu Glu Glu Asn Ile Val Ile Leu Ser Lys Gln Val Glu
 260 265 270
 Asp Leu Asn Val Lys Cys Gln Leu Leu Glu Lys Glu Lys Glu Asp His
 275 280 285
 Val Asn Arg Asn Arg Glu His Asn Glu Asn Leu Asn Ala Glu Met Gln
 290 295 300
 Asn Leu Lys Gln Lys Phe Ile Leu Glu Gln Gln Glu Arg Glu Lys Leu
 305 310 315 320
 Gln Gln Lys Glu Leu Gln Ile Asp Ser Leu Leu Gln Gln Glu Lys Glu
 325 330 335
 Leu Ser Ser Leu His Gln Lys Leu Cys Ser Phe Gln Glu Glu Met
 340 345 350
 Val Lys Glu Lys Asn Leu Phe Glu Glu Glu Leu Lys Gln Thr Leu Asp
 355 360 365
 Glu Leu Asp Lys Leu Gln Gln Lys Glu Glu Gln Ala Glu Arg Leu Val
 370 375 380
 Lys Gln Leu Glu Glu Ala Lys Ser Arg Ala Glu Glu Leu Lys Leu
 385 390 395 400
 Leu Glu Glu Lys Leu Lys Gly Lys Glu Ala Glu Leu Glu Lys Ser Ser
 405 410 415
 Ala Ala His Thr Gln Ala Thr Leu Leu Gln Glu Lys Tyr Asp Ser
 420 425 430
 Met Val Gln Ser Leu Glu Asp Val Thr Ala Gln Phe Glu Ser Tyr Lys
 435 440 445
 Ala Leu Thr Ala Ser Glu Ile Glu Asp Leu Lys Leu Glu Asn Ser Ser
 450 455 460
 Leu Gln Glu Lys Ala Ala Lys Ala Gly Lys Asn Ala Glu Asp Val Gln
 465 470 475 480
 His Gln Ile Leu Ala Thr Glu Ser Ser Asn Gln Glu Tyr Val Arg Met
 485 490 495
 Leu Leu Asp Leu Gln Thr Lys Ser Ala Leu Lys Glu Thr Glu Ile Lys
 500 505 510
 Glu Ile Thr Val Ser Phe Leu Gln Lys Ile Thr Asp Leu Gln Asn Gln
 515 520 525
 Leu Lys Gln Gln Glu Glu Asp Phe Arg Lys Gln Leu Glu Asp Glu Glu
 530 535 540
 Gly Arg Lys Ala Glu Lys Glu Asn Thr Thr Ala Glu Leu Thr Glu Glu
 545 550 555 560
 Ile Asn Lys Trp Arg Leu Leu Tyr Glu Glu Leu Tyr Asn Lys Thr Lys
 565 570 575
 Pro Phe Gln Leu Gln Leu Asp Ala Phe Glu Val Glu Lys Gln Ala Leu
 580 585 590
 Leu Asn Glu His Gly Ala Ala Gln Glu Gln Leu Asn Lys Ile Arg Asp
 595 600 605
 Ser Tyr Ala Lys Leu Leu Gly His Gln Asn Leu Lys Gln Lys Ile Lys
 610 615 620
 His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser Glu Val
 625 630 635 640

Ser Lys Leu Arg Cys Gln Leu Ala Lys Lys Gln Ser Glu Thr Lys
 645 650 655
 Leu Gln Glu Glu Leu Asn Lys Val Leu Gly Ile Lys His Phe Asp Pro
 660 665 670
 Ser Lys Ala Phe His His Glu Ser Lys Glu Asn Phe Ala Leu Lys Thr
 675 680 685
 Pro Leu Lys Glu Gly Asn Thr Asn Cys Tyr Arg Ala Pro Met Glu Cys
 690 695 700
 Gln Glu Ser Trp Lys
 705

<210> 14
 <211> 2957
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 14

gccagtcacc	ttcagttct	ggagctggcc	gtcaacatgt	ccttcctaa	ggcgcccttg	60
aaacgattca	atgacccttc	tggttgtgca	ccatctccag	gtgcttatga	tgttaaaact	120
ttagaagtat	tgaaaggacc	agtatcctt	cagaaaatcac	aaagattaa	acaacaaaaa	180
gaatctaaac	aaaatcttaa	tgttgcacaaa	gatactacct	tgcctgcttc	agctagaaaaa	240
gttaagtctt	cggaatcaaa	gattcgtgtt	cttctacagg	aacgtgtgc	ccaggacagc	300
cggatccagg	atctggaaac	tgagttggaa	aagatggaag	caaggctaaa	tgtgcacta	360
agggaaaaaa	catctctctc	tgcaataat	gctacactgg	aaaaacaact	tattgaattt	420
accaggacta	atgaactact	aaaatctaag	tttctgaaa	atggtaacca	gaagaatttt	480
agaattctaa	gcttggagtt	gatgaaactt	agaaacaaaa	gagaaacaaa	gatgaggggt	540
atgatggcta	agcaagaagg	catggagatg	aagctgcagg	tcacccaaag	gagtctcgaa	600
gagtctcaag	ggaaaatagc	ccaactggag	ggaaaacttg	tttcaataga	gaaagaaaag	660
attgtgaaa	aatctgaaac	agaaaaactc	ttgaaataca	tcgaagaaat	tagttgtgt	720
tcagatcaag	tggaaaaata	caagctagat	attgcccagt	tagaagaaaa	tttggaaagag	780
aagaatgatg	aaattttaag	ccttaagcag	tctcttgagg	agaatattgt	tatattatct	840
aaacaagtag	aagatctaaa	tgtgaaatgt	cagctgcttgc	aaaaagaaaa	agaagaccat	900
gtcaacagga	atagagaaca	caacgaaaat	ctaaatgcag	agatgcaaaa	cttaaaacag	960
aagtttattc	ttgaaacaaca	ggaacgtgaa	aagcttcaac	aaaaagaatt	acaaattgtat	1020
tcacttctgc	aacaagagaa	agaatttatct	tcgagtcttc	atcagaagct	ctgttctttt	1080
caagaggaaa	tggttaaaga	gaagaatctg	tttgaggaag	aattaaagca	aacactggat	1140
gagcttgata	aattacagca	aaaggaggaa	caagctgaaa	ggctggtaa	gaaattggaa	1200
gaggaagcaa	aatcttagagc	tgaagaatta	aaactcctag	aagaaaaagct	gaaagggaaag	1260
gaggctgaac	tggagaaaag	tagtgcgt	catacccagg	ccaccctgc	tttgcaggaa	1320
aagtatgaca	gtatggtgca	aagcctgaa	gatgttactg	ctcaatttga	aagctaaaa	1380
gcgttaacag	ccagttagat	agaagatctt	aagctggaga	actcatcatt	acaggaaaaa	1440
gcggccaagg	ctggggaaaaa	tgcagaggat	gttcagcatc	agattttggc	aactgagagc	1500
tcaaatacag	aatatgtaaag	gatgcttctt	gatctgcaga	ccaaagtgc	actaaaggaa	1560
acagaaaatta	aagaaatcac	agtttctttt	cttcaaaaaaa	taactgattt	gcagaaccaa	1620
ctcaagcaac	aggaggaaaga	cttttagaaaa	cagctggaaag	atgaagaagg	aagaaaaagct	1680
aaaaaaagaaa	ataacaacagc	agaattaact	gaagaaattta	acaagtggcg	tccctcttat	1740
gaagaactat	ataataaaaac	aaaacctttt	cagctacaac	tagatgttt	tgaagtagaa	1800
aaacaggcat	tgttgaatga	acatggtgca	gctcagggaaac	agctaaataa	aataagagat	1860
tcatatgcta	aattatttgg	tcatcagaat	ttgaaacaaa	aatcaagca	tgttgtgaag	1920
ttgaaagatg	aaaatagcca	actcaaatcg	gaagtatcaa	aactccgctg	tcagcttgct	1980
aaaaaaaaaac	aaagttagac	aaaacttcaa	gagaattga	ataaaaggct	aggtatcaaa	2040
cactttgatc	cttcaaaaggc	tttcatcat	gaaagtaaag	aaaatttgc	cctgaagacc	2100
ccattaaaag	aaggcaataac	aaaactgttac	cgagctceta	tggagtgta	agaatcatgg	2160
aagtaaacat	ctgagaaacc	tgttgaagat	tatttcattc	gtcttgggt	tattgtatgtt	2220
gctgttatta	tatttgacat	gggtatttta	taatgttgta	ttaatttta	actgccaatc	2280
cttaaatatg	tgaaaggaac	atttttacc	aaagtgttctt	ttgacatttt	attttttctt	2340
gcaaatacct	cctcccttaat	gctcaccttt	atcacctcat	tctgacccct	ttcgctggct	2400

tccagctta	aatgcac	tatcaactt	aaagtcagta	tcatattatt	atccctcctgt	2460
tctgaaacct	tagttcaag	agtctaaacc	ccagattctt	cagcttgc	ctggaggct	2520
tttctagtct	gagcttctt	agctaggcta	aaacaccc	gcttgttatt	gcctctactt	2580
tgattctgat	aatgctca	tggcctacc	tattatc	ctacttgtcc	agttcaaata	2640
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atttacaggt	tcttaggctc	catcctgtt	gtatgaaatt	ataatctgtg	gattggc	2760
taagcctgca	ttcttaacaa	actcttc	taattcttag	atacactaaa	aatctgagaa	2820
actctacatg	taactatttc	ttcagagttt	gtcatatact	gcttgtcatc	tgcatgtcta	2880
ctcagcattt	gattaacatt	tgtgtat	gaaataaaat	tacacagtaa	gtcatttaac	2940
caaaaaaaaaa	aaaaaaaaaa					2957

<210> 15
<211> 725
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 15
Met Ser Phe Pro Lys Ala Pro Leu Lys Arg Phe Asn Asp Pro Ser Gly

1	5	10	15													
Cys	Ala	Pro	Ser	Pro	Gly	Ala	Tyr	Asp	Val	Lys	Thr	Leu	Glu	Val	Leu	
20							25							30		
Lys	Gly	Pro	Val	Ser	Phe	Gln	Lys	Ser	Gln	Arg	Phe	Lys	Gln	Gln	Lys	
35							40							45		
Glu	Ser	Lys	Gln	Asn	Leu	Asn	Val	Asp	Lys	Asp	Thr	Thr	Leu	Pro	Ala	
50							55							60		
Ser	Ala	Arg	Lys	Val	Lys	Ser	Ser	Glu	Ser	Lys	Glu	Ser	Gln	Lys		
65							70							80		
Asn	Asp	Lys	Asp	Leu	Lys	Ile	Leu	Glu	Lys	Glu	Ile	Arg	Val	Leu	Leu	
85							90							95		
Gln	Glu	Arg	Gly	Ala	Gln	Asp	Arg	Arg	Ile	Gln	Asp	Leu	Glu	Thr	Glu	
100							105							110		
Leu	Glu	Lys	Met	Glu	Ala	Arg	Leu	Asn	Ala	Ala	Leu	Arg	Glu	Lys	Thr	
115							120							125		
Ser	Leu	Ser	Ala	Asn	Asn	Ala	Thr	Leu	Glu	Lys	Gln	Leu	Ile	Glu	Leu	
130							135							140		
Thr	Arg	Thr	Asn	Glu	Leu	Leu	Lys	Ser	Lys	Phe	Ser	Glu	Asn	Gly	Asn	
145							150							160		
Gln	Lys	Asn	Leu	Arg	Ile	Leu	Ser	Leu	Glu	Leu	Met	Lys	Leu	Arg	Asn	
165							170							175		
Lys	Arg	Glu	Thr	Lys	Met	Arg	Gly	Met	Met	Ala	Lys	Gln	Glu	Gly	Met	
180							185							190		
Glu	Met	Lys	Leu	Gln	Val	Thr	Gln	Arg	Ser	Leu	Glu	Glu	Ser	Gln	Gly	
195							200							205		
Lys	Ile	Ala	Gln	Leu	Glu	Gly	Lys	Leu	Val	Ser	Ile	Glu	Lys	Glu	Lys	
210							215							220		
Ile	Asp	Glu	Lys	Ser	Glu	Thr	Glu	Lys	Leu	Leu	Glu	Tyr	Ile	Glu	Glu	
225							230							235		240
Ile	Ser	Cys	Ala	Ser	Asp	Gln	Val	Glu	Lys	Tyr	Lys	Leu	Asp	Ile	Ala	
245														250		255
Gln	Leu	Glu	Glu	Asn	Leu	Lys	Glu	Lys	Asn	Asp	Glu	Ile	Leu	Ser	Leu	
260							265							270		
Lys	Gln	Ser	Leu	Glu	Asp	Asn	Ile	Val	Ile	Leu	Ser	Lys	Gln	Val	Glu	
275							280							285		
Asp	Leu	Asn	Val	Lys	Cys	Gln	Leu	Leu	Glu	Thr	Glu	Lys	Glu	Asp	His	
290							295							300		

Val Asn Arg Asn Arg Glu His Asn Glu Asn Leu Asn Ala Glu Met Gln
 305 310 315 320
 Asn Leu Glu Gln Lys Phe Ile Leu Glu Gln Arg Glu His Glu Lys Leu
 325 330 335
 Gln Gln Lys Glu Leu Gln Ile Asp Ser Leu Leu Gln Gln Glu Lys Glu
 340 345 350
 Leu Ser Ser Ser Leu His Gln Lys Leu Cys Ser Phe Gln Glu Glu Met
 355 360 365
 Val Lys Glu Lys Asn Leu Phe Glu Glu Glu Leu Lys Gln Thr Leu Asp
 370 375 380
 Glu Leu Asp Lys Leu Gln Gln Lys Glu Glu Gln Ala Glu Arg Leu Val
 385 390 395 400
 Lys Gln Leu Glu Glu Ala Lys Ser Arg Ala Glu Glu Leu Lys Leu
 405 410 415
 Leu Glu Glu Lys Leu Lys Gly Lys Glu Ala Glu Leu Glu Lys Ser Ser
 420 425 430
 Ala Ala His Thr Gln Ala Thr Leu Leu Leu Gln Glu Lys Tyr Asp Ser
 435 440 445
 Met Val Gln Ser Leu Glu Asp Val Thr Ala Gln Phe Glu Ser Tyr Lys
 450 455 460
 Ala Leu Thr Ala Ser Glu Ile Glu Asp Leu Lys Leu Glu Asn Ser Ser
 465 470 475 480
 Leu Gln Glu Lys Ala Ala Lys Ala Gly Lys Asn Ala Glu Asp Val Gln
 485 490 495
 His Gln Ile Leu Ala Thr Glu Ser Ser Asn Gln Glu Tyr Val Arg Met
 500 505 510
 Leu Leu Asp Leu Gln Thr Lys Ser Ala Leu Lys Glu Thr Glu Ile Lys
 515 520 525
 Glu Ile Thr Val Ser Phe Leu Gln Lys Ile Thr Asp Leu Gln Asn Gln
 530 535 540
 Leu Lys Gln Gln Glu Glu Asp Phe Arg Lys Gln Leu Glu Asp Glu Glu
 545 550 555 560
 Gly Arg Lys Ala Glu Lys Glu Asn Thr Thr Ala Glu Leu Thr Glu Glu
 565 570 575
 Ile Asn Lys Trp Arg Leu Leu Tyr Glu Glu Leu Tyr Asn Lys Thr Lys
 580 585 590
 Pro Phe Gln Leu Gln Leu Asp Ala Phe Glu Val Glu Lys Gln Ala Leu
 595 600 605
 Leu Asn Glu His Gly Ala Ala Gln Glu Gln Leu Asn Lys Ile Arg Asp
 610 615 620
 Ser Tyr Ala Lys Leu Leu Gly His Gln Asn Leu Lys Gln Lys Ile Lys
 625 630 635 640
 His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser Glu Val
 645 650 655
 Ser Lys Leu Arg Cys Gln Leu Ala Lys Lys Gln Ser Glu Thr Lys
 660 665 670
 Leu Gln Glu Glu Leu Asn Lys Val Leu Gly Ile Lys His Phe Asp Pro
 675 680 685
 Ser Lys Ala Phe His His Glu Ser Lys Glu Asn Phe Ala Leu Lys Thr
 690 695 700
 Pro Leu Lys Glu Gly Asn Thr Asn Cys Tyr Arg Ala Pro Met Glu Cys
 705 710 715 720
 Gln Glu Ser Trp Lys
 725

<210> 16

<211> 2756

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 16

tcgagcggcc	gcccgggcag	gtgtgccagt	caccctcagt	ttctggagct	ggccgtcaac	60
atgtccttgc	ctaaggcgcc	cttgaacacga	ttcaatgacc	cttctgggttgc	tgaccatct	120
ccaggtgctt	atgatgttaa	aactttagaa	gtattgaaag	gaccagtatc	ctttcagaaa	180
tcacaaagat	ttaaacaaca	aaaagaatct	aaacaaaatc	ttaatgttga	caaagatact	240
accttgcctg	cttcagctag	aaaagttaag	tcttcggaat	caaagaagga	atctcaaaaag	300
aatgataaag	atttgaagat	attagagaaa	gagattcgtg	ttcttctaca	ggaacgtggt	360
gcccaggaca	ggcggatcca	ggatctggaa	actgagttgg	aaaagatgga	agcaaggcta	420
aatgtgcac	taaggaaaaa	aacatctctc	tctgcaaata	atgctacact	ggaaaaaaca	480
cttattgaat	tgaccaggac	taatgaacta	ctaaaatcta	agtttctga	aaatggtaac	540
cagaagaatt	tgagaattct	aagcttggag	ttgatgaaac	ttagaaacaa	aagagaaaaca	600
aagatgaggg	gtatgatggc	taagcaagaa	ggcatggaga	tgaagctgca	ggtcacccaa	660
aggagtctcg	aagagtctca	agggaaaaata	gcccaactgg	agggaaaaact	tgtttcaata	720
gagaaagaaa	agattgatga	aaaatctgaa	acagaaaaac	tcttggata	catcgaagaa	780
attagttgtg	cttcagatca	agtggaaaaaa	tacaagctag	atattgccc	gttagaagaa	840
aatttgaag	agaagaatga	tgaaattttta	agcctaagc	agtcttttga	ggacaatatt	900
gttatattat	ctaaacaagt	agaagatcta	aatgtgaaat	gtcagctgct	tgaaacagaa	960
aaagaagacc	atgtcaacag	gaatagagaa	cacaacgaaa	atctaaatgc	agagatgcaa	1020
aacttagaac	agaagtttat	tcttgaacaa	cgggaacatg	aaaagcttca	acaaaaagaa	1080
ttacaaatttgc	attcacttct	gcaacaagag	aaagaattat	cttcgagttc	tcatcagaag	1140
ctctgttctt	ttcaagagga	aatggttaaa	gagaagaatc	tgtttgagga	agaattaaag	1200
caaacactgg	atgagcttgc	taaatttacag	caaaaaggagg	aacaagctga	aaggctggtc	1260
aagcaattgg	aagaggaagc	aaaatctaga	gctgaagaat	taaaactcct	agaagaaaaag	1320
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cgtctcctct	atgaagaact	atataataaa	acaaaacattt	ttcagctaca	actagatgt	1860
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tgccctact	ttgatttttgc	ataatgttca	cttgccttca	cctattatcc	tttctacttgc	2700
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<210> 17

<211> 59

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 17

Asp Ser Tyr Ala Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys Ile
1 5 10 15
Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser Glu
20 25 30
Val Ser Lys Leu Arg Ser Gln Leu Val Lys Arg Lys Gln Asn Glu Leu
35 40 45
Arg Leu Gln Gly Glu Leu Asp Lys Ala Leu Gly
50 55

<210> 18

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 18

Arg Asp Ser Tyr Ala Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys
1 5 10 15
Ile Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser
20 25 30
Glu Val Ser Lys Leu Arg Ser Gln Leu Val Lys Arg Lys Gln Asn Glu
35 40 45
Leu Arg Leu Gln Gly Glu Leu Asp Lys Ala Leu Gly
50 55 60

<210> 19

<211> 59

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 19

Arg Asp Ser Tyr Ala Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys
1 5 10 15
Ile Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser
20 25 30
Glu Val Ser Lys Leu Arg Ser Gln Leu Lys Arg Lys Gln Asn Glu Leu
35 40 45
Arg Leu Gln Gly Glu Leu Asp Lys Ala Leu Gly
50 55

<210> 20

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 20

Arg Asp Ser Tyr Ala Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys
1 5 10 15

Ile Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser
20 25 30
Glu Val Ser Lys Leu Arg Ser Gln Leu Ala Lys Arg Lys Gln Asn Glu
35 40 45
Leu Arg Leu Gln Gly Glu Leu Asp Lys Ala Leu Gly
50 55 60

<210> 21
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 21
Arg Asp Ser Tyr Ala Leu Leu Gly His Gln Asn Leu Lys Gln Lys Ile
1 5 10 15
Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser Glu
20 25 30
Val Ser Lys Leu Arg Gln Leu Lys Lys Gln Glu Leu Gln Glu Leu Lys
35 40 45
Leu Gly
50

<210> 22
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 22
Arg Asp Ser Tyr Ala Lys Leu Leu Gly His Gln Asn Leu Lys Gln Lys
1 5 10 15
Ile Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser
20 25 30
Glu Val Ser Lys Leu Arg Cys Gln Leu Ala Lys Lys Lys Gln Ser Glu
35 40 45
Thr Lys Leu Gln Glu Glu Leu Asn Lys Val Leu Gly
50 55 60

<210> 23
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 23
Arg Asp Ser Tyr Ala Leu Leu Gly His Gln Asn Leu Lys Gln Lys Ile
1 5 10 15
Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Leu Lys Ser Glu Val
20 25 30
Lys Leu Arg Gln Leu Lys Arg Lys Gln Glu Leu Gln Glu Leu Lys Leu
35 40 45

Gly

<210> 24
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 24
Arg Asp Ser Tyr Ala Lys Leu Leu Gly His Gln Asn Leu Lys Gln Lys
1 5 10 15
Ile Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Asn Leu Lys Ser
20 25 30
Glu Val Leu Lys Leu Arg Ala Gln Leu Thr Lys Arg Lys Gln Ser Glu
35 40 45
Ala Lys Leu Gln Glu Glu Leu Asn Lys Val Leu Gly
50 55 60

<210> 25
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 25
Ser Tyr Ala Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys Ile Lys
1 5 10 15
His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser Glu Val
20 25 30
Ser Lys Leu Arg Ser Gln Leu Val Lys Arg Lys Gln Asn Glu Leu Arg
35 40 45
Leu Gln
50

<210> 26
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 26
Tyr Ala Leu Gly His Gln Asn Gln Lys Ile Lys His Val Lys Leu Lys
1 5 10 15
Glu Asn Leu Lys Glu Val Ser Lys Leu Arg Ser Gln Lys Lys Gln Arg
20 25 30
Leu

<210> 27
<211> 50
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 27

Ala Tyr Ala Asn Leu Met Gly His Gln Asn Gln Arg Gln Lys Ile Lys
1 5 10 15
His Met Val Lys Leu Lys Glu Glu Asn Leu Glu Leu Lys Gln Glu Val
20 25 30
Ser Lys Leu Arg Ser Gln Val Gly Lys Gln Lys Gln Glu Leu Asp Arg
35 40 45
Leu Lys
50

<210> 28

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 28

Arg Asp Ser Tyr Ala Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys
1 5 10 15
Ile Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser
20 25 30

<210> 29

<211> 33

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 29

Leu Lys Ser Glu Val Ser Lys Leu Arg Ser Gln Leu Val Lys Arg Lys
1 5 10 15
Gln Asn Glu Leu Arg Leu Gln Gly Glu Leu Asp Lys Ala Leu Gly Ile
20 25 30
Arg

<210> 30

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 30

Leu Glu Val Ser Lys Leu Arg Ser Gln Leu Val Lys Arg Lys Gln Asn
1 5 10 15

Glu Leu Arg Leu Gln Gly Glu Leu Asp Lys Ala Leu Gly Ile Arg
20 25 30

<210> 31
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 31
Leu Ser Gln Glu Val Ser Lys Leu Arg Ser Gln Leu Val Lys Arg Lys
1 5 10 15
Gln Asn Glu Leu Arg Leu Gln Gly Glu Leu Asp Lys Ala Leu Gly Ile
20 25 30
Arg

<210> 32
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 32
Arg Asp Ser Tyr Ala Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys
1 5 10 15
Ile Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser
20 25 30
Glu Val Ser Lys Leu Arg Ser Gln Leu Val Lys
35 40

<210> 33
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 33
Arg Asp Ser Tyr Ala Leu Leu Gly His Gln Asn Leu Lys Gln Lys Ile
1 5 10 15
Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser Val
20 25 30
Lys Lys

<210> 34
<211> 42
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 34

Arg Asp Ser Tyr Ala Lys Leu Leu Gly His Gln Asn Leu Lys Gln Lys
1 5 10 15
Ile Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser
20 25 30
Val Cys Lys Met Thr Phe His Phe Ile Lys
35 40

<210> 35

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 35

Glu Val Ser Lys Leu Arg Ser Gln Leu Val Lys Arg Lys Gln Asn Glu
1 5 10 15
Leu Arg Leu Gln Gly Glu Leu Asp Lys Ala Leu Gly Ile Arg
20 25 30

<210> 36

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 36

Glu Val Ser Lys Leu Arg Gln Leu Lys Lys Gln Glu Leu Gln Glu Leu
1 5 10 15
Lys Leu Gly Ile
20

<210> 37

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 37

Glu Val Ser Lys Leu Arg Cys Gln Leu Ala Lys Lys Lys Gln Ser Glu
1 5 10 15
Thr Lys Leu Gln Glu Glu Leu Asn Lys Val Leu Gly Ile Lys
20 25 30

<210> 38

<211> 28

<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 38
Tyr Ala Leu Leu Gly His Gln Asn Lys Gln Lys Ile His Lys Lys Asp
1 5 10 15
Glu Asn Leu Lys Glu Val Lys Leu Arg Lys Asn Gly
20 25

<210> 39
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 39
Asn Asp Tyr Ala Lys Leu Leu Gly His Gln Asn Gln Lys Gln Lys Ile
1 5 10 15
His His Ile Met Lys Ile Lys Asp Glu Asn Ala Ser Leu Lys Lys Glu
20 25 30
Val Thr Lys Leu Arg Glu Glu Thr Thr Lys Gln Ser Arg Asn Leu Arg
35 40 45
Gln Met Lys Asp Lys Val Glu Lys Met Glu Gly
50 55

<210> 40
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 40
Asp Ser Tyr Ala Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys Ile
1 5 10 15
Lys His Val Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys
20 25 30

<210> 41
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 41
Asp Tyr Ala Leu Gly His Gln Asn Gln Lys Ile Lys His Val Lys Leu
1 5 10 15
Lys Glu Asn Leu Lys
20

<210> 42
<211> 30

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 42
Asp Ala Tyr Ala Asn Leu Met Gly His Gln Asn Gln Arg Gln Lys Ile
1 5 10 15
Lys His Met Val Lys Leu Lys Glu Glu Asn Leu Glu Leu Lys
20 25 30

<210> 43

<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 43
Glu Val Ser Lys Leu Arg Ser Gln Leu Val Lys Arg Lys Gln Asn Glu
1 5 10 15
Leu Arg Leu Gln
20

<210> 44
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 44
Glu Val Ser Lys Leu Arg Ser Gln Lys Lys Gln Arg Leu
1 5 10

<210> 45
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 45
Glu Val Ser Lys Leu Arg Ser Gln Val Gly Lys Gln Lys Gln Glu Leu
1 5 10 15
Asp Arg Leu Lys
20

<210> 46
<211> 43
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 46

Gln	Leu	Leu	Gly	His	Gln	Asn	Leu	Lys	Gln	Lys	Ile	Lys	His	Val	Val
1					5				10				15		
Lys	Leu	Lys	Asp	Glu	Asn	Ser	Gln	Leu	Lys	Ser	Glu	Val	Ser	Lys	Leu
					20				25				30		
Arg	Ser	Gln	Leu	Val	Lys	Arg	Lys	Gln	Asn	Glu					
					35				40						

<210> 47

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 47

Leu	Gly	His	Gln	Asn	Leu	Gln	Lys	Ile	Val	Val	Leu	Lys	Glu	Asn	Leu
1					5				10				15		
Glu	Lys	Leu	Arg	Val	Lys										
					20										

<210> 48

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 48

Lys	Leu	Ile	Gly	His	Gln	Asn	Leu	His	Gln	Lys	Ile	Gln	Tyr	Val	Val
1								5		10			15		
Arg	Leu	Lys	Lys	Glu	Asn	Ile	Arg	Leu	Ala	Glu	Glu	Thr	Glu	Lys	Leu
								20		25			30		
Arg	Ala	Glu	Asn	Val	Phe	Leu	Lys	Glu	Arg	Lys					
					35				40						

<210> 49

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 49

Leu	Gly	His	Gln	Asn	Leu	Gln	Lys	Ile	Val	Val	Leu	Lys	Glu	Asn	Leu
1								5		10			15		
Glu	Lys	Leu	Arg	Val	Lys										
					20										

<210> 50

<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 50
Lys Leu Val Gly His Gln Asn Leu His Gln Lys Ile Gln Tyr Val Val
1 5 10 15
Arg Leu Lys Lys Glu Asn Val Arg Leu Ala Glu Glu Thr Glu Lys Leu
20 25 30
Arg Ala Glu Asn Val Phe Leu Lys Glu Lys Lys
35 40

<210> 51
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 51
Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys Ile Lys His Val Val
1 5 10 15
Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser Glu Val Ser Lys Leu
20 25 30
Arg Ser Gln Leu Val Lys Arg Lys Gln Asn Glu
35 40

<210> 52
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 52
Leu Gly His Gln Asn Leu Gln Lys Ile Val Val Leu Lys Glu Asn Leu
1 5 10 15
Glu Lys Leu Arg Lys Lys Glu
20

<210> 53
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 53
Lys Leu Val Gly His Gln Asn Leu His Gln Lys Ile Gln Tyr Val Val
1 5 10 15

Arg Leu Lys Lys Glu Asn Ile Arg Leu Thr Glu Glu Thr Glu Lys Leu
20 25 30

Arg Ala Glu Asn Leu Phe Leu Lys Glu Lys Lys Lys Glu
35 40 45

<210> 54

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 54

Leu Gly His Gln Asn Gln Lys Ile Val Lys Leu Lys Glu Asn Leu Glu
1 5 10 15
Lys Leu Arg Lys
20

<210> 55

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 55

Lys Ile Leu Gly His Gln Asn Pro Asn Gln Lys Ile Gln Tyr Leu Val
1 5 10 15
Lys Leu Lys Lys Glu Asn Asn Lys Leu Leu Glu Glu Ala Glu Lys Leu
20 25 30
Arg Ile Glu Asn Leu Phe Leu Lys Glu Ser Lys
35 40

<210> 56

<211> 51

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 56

Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys Ile Lys His Val Val
1 5 10 15
Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser Glu Val Ser Lys Leu
20 25 30
Arg Ser Gln Leu Val Lys Arg Lys Gln Asn Glu Leu Arg Leu Gln Gly
35 40 45
Glu Leu Asp
50

<210> 57

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 57

Leu Gly His Gln Asn Lys Gln Lys Ile His Lys Glu Asn Leu Lys Glu
1 5 10 15
Val Leu Gln Leu Lys
20

<210> 58

<211> 51

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 58

Glu Leu Gly Gly His Gln Asn Pro Lys Gln Lys Ile His His Leu Gln
1 5 10 15
Ala Val Lys Ser Glu Asn Tyr Phe Leu Lys Glu Glu Val Glu Ser Leu
20 25 30
Glu Lys Gln Leu Gly Lys Ala Gln Ser Asp Ser Glu Gln Met Lys Arg
35 40 45
Asp Tyr Glu
50

<210> 59

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 59

Gln Leu Leu Gly His Gln Asn Leu Lys Gln Lys Ile Lys His Val Val
1 5 10 15
Lys Leu Lys Asp Glu Asn Ser Gln Leu
20 25

<210> 60

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 60

Leu Gly His Gln Asn Leu Gln Lys Ile Val Val Leu Lys Glu Asn Leu
1 5 10 15

<210> 61

<211> 25

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 61
Lys Leu Val Gly His Gln Asn Leu His Gln Lys Ile Gln Tyr Val Val
1 5 10 15
Arg Leu Lys Lys Glu Asn Val Arg Leu
20 25

<210> 62
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 62
Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser Glu Val Ser Lys
1 5 10 15
Leu Arg Ser Gln Leu Val Lys Arg Lys Gln Asn Glu Leu Arg
20 25 30

<210> 63
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 63
Val Lys Leu Glu Asn Leu Lys Lys Leu Leu Lys Gln Glu Arg
1 5 10

<210> 64
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 64
Val Lys Leu Glu Glu Asn Arg Ser Leu Lys Ala Asp Leu Gln Lys
1 5 10 15
Leu Lys Asp Glu Leu Ala Ser Thr Lys Gln Ser Glu Ala Arg
20 25 30

<210> 65
<211> 28
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 65

Val Lys Leu Lys Asp Glu Asn Ser Gln Leu Lys Ser Glu Val Ser Lys
1 5 10 15
Leu Arg Ser Gln Leu Val Lys Arg Lys Gln Asn Glu
20 25

<210> 66

<211> 14
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 66

Val Lys Leu Glu Asn Leu Lys Glu Lys Leu Leu Lys Gln Glu
1 5 10

<210> 67

<211> 28
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 67

Val Lys Leu Glu Glu Asn Arg Ser Leu Lys Ala Glu Leu Gln Lys
1 5 10 15
Leu Lys Asp Glu Leu Ala Ser Thr Lys Gln Ser Glu
20 25